

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/735,863

Source: _____

Date Processed by STIC: _____

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 12/01/2004

PATENT APPLICATION: US/10/735,863

TIME: 12:33:43

Input Set : N:\Crf3\RULE60\10735863.raw.txt

Output Set: N:\CRF4\12012004\J735863.raw

```

1 <110> APPLICANT: Brettman, Lee R.
2   Fox, Judith A.
3   Allison, David Edward
4 <120> TITLE OF INVENTION: Method of Administering an Antibody
5 <130> FILE REFERENCE: 1855.2007-001
6 <140> CURRENT APPLICATION NUMBER: US/10/735,863
7 <141> CURRENT FILING DATE: 2003-12-15
8 <150> PRIOR APPLICATION NUMBER: US/09/748,960
9 <151> PRIOR FILING DATE: 2000-12-27
10 <150> PRIOR APPLICATION NUMBER: US 09/550,082
11 <151> PRIOR FILING DATE: 2000-04-14
12 <160> NUMBER OF SEQ ID NOS: 16
13 <170> SOFTWARE: FastSEQ for Windows Version 4.0
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 396
17 <212> TYPE: DNA
18 <213> ORGANISM: Mus musculus
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (1)...(396)
22 <400> SEQUENCE: 1
23   atg aag ttg cct gtt agg ctg ttg gtg ctt ctg ttg ttc tgg att cct   48
24   Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Phe Trp Ile Pro
25     1             5             10             15
26   gtt tcc gga ggt gat gtt gtg gtg act caa act cca ctc tcc ctg cct   96
27   Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
28     20             25             30
29   gtc agc ttt gga gat caa gtt tct atc tct tgc agg tct agt cag agt   144
30   Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
31     35             40             45
32   ctt gca aag agt tat ggg aac acc tat ttg tct tgg tac ctg cac aag   192
33   Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys
34     50             55             60
35   cct ggc cag tct cca cag ctc ctc atc tat ggg att tcc aac aga ttt   240
36   Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
37     65             70             75             80
38   tct ggg gtg cca gac agg ttc agt ggc agt ggt tca ggg aca gat ttc   288
39   Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
40     85             90             95
41   aca ctc aag atc agc aca ata aag cct gag gac ttg gga atg tat tac   336
42   Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
43     100            105            110
44   tgc tta caa ggt aca cat cag ccg tac acg ttc gga ggg ggg acc aag   384

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45      Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys
46              115                      120                      125
47      ctg gaa ata aaa
48      Leu Glu Ile Lys
49              130
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 132
53 <212> TYPE: PRT
54 <213> ORGANISM: Mus musculus
55 <220> FEATURE:
56 <221> NAME/KEY: SIGNAL
57 <222> LOCATION: (1)...(20)
58 <223> OTHER INFORMATION: signal peptide
59 <220> FEATURE:
60 <221> NAME/KEY: SITE
61 <222> LOCATION: (21)...(43)
62 <223> OTHER INFORMATION: framework 1
63 <220> FEATURE:
64 <221> NAME/KEY: SITE
65 <222> LOCATION: (44)...(59)
66 <223> OTHER INFORMATION: CDR1
67 <220> FEATURE:
68 <221> NAME/KEY: SITE
69 <222> LOCATION: (60)...(74)
70 <223> OTHER INFORMATION: framework 2
71 <220> FEATURE:
72 <221> NAME/KEY: SITE
73 <222> LOCATION: (75)...(81)
74 <223> OTHER INFORMATION: CDR2
75 <220> FEATURE:
76 <221> NAME/KEY: SITE
77 <222> LOCATION: (82)...(113)
78 <223> OTHER INFORMATION: framework 3
79 <220> FEATURE:
80 <221> NAME/KEY: SITE
81 <222> LOCATION: (114)...(122)
82 <223> OTHER INFORMATION: CDR3
83 <220> FEATURE:
84 <221> NAME/KEY: SITE
85 <222> LOCATION: (123)...(132)
86 <223> OTHER INFORMATION: framework 4
87 <400> SEQUENCE: 2
88      Met Lys Leu Pro Val Arg Leu Leu Val Leu Leu Leu Phe Trp Ile Pro
89              1              5              10              15
90      Val Ser Gly Gly Asp Val Val Val Thr Gln Thr Pro Leu Ser Leu Pro
91              20              25              30
92      Val Ser Phe Gly Asp Gln Val Ser Ile Ser Cys Arg Ser Ser Gln Ser
93              35              40              45
94      Leu Ala Lys Ser Tyr Gly Asn Thr Tyr Leu Ser Trp Tyr Leu His Lys

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```

95          50          55          60
96    Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gly Ile Ser Asn Arg Phe
97    65          70          75          80
98    Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
99          85          90          95
100    Thr Leu Lys Ile Ser Thr Ile Lys Pro Glu Asp Leu Gly Met Tyr Tyr
101          100          105          110
102    Cys Leu Gln Gly Thr His Gln Pro Tyr Thr Phe Gly Gly Gly Thr Lys
103          115          120          125
104    Leu Glu Ile Lys
105          130
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 420
109 <212> TYPE: DNA
110 <213> ORGANISM: Mus musculus
111 <220> FEATURE:
112 <221> NAME/KEY: CDS
113 <222> LOCATION: (1)...(420)
114 <400> SEQUENCE: 3
115    atg gga tgg agc tgt atc atc ctc ttc ttg gta tca aca gct aca agt    48
116    Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
117    1          5          10          15
118    gtc cac tcc cag gtc caa ctg cag cag cct ggg gct gag ctt gtg aag    96
119    Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
120          20          25          30
121    cct ggg act tca gtg aag ctg tcc tgc aag ggt tat ggc tac acc ttc    144
122    Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
123          35          40          45
124    acc agc tac tgg atg cac tgg gtg aag cag agg cct gga caa ggc ctt    192
125    Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
126    50          55          60
127    gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat    240
128    Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
129    65          70          75          80
130    caa aaa ttc aag ggc aag gcc aca ttg act gta gac att tcc tcc agc    288
131    Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
132          85          90          95
133    aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc    336
134    Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
135          100          105          110
136    tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac    384
137    Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
138          115          120          125
139    tac tgg ggt caa ggc acc tca gtc acc gtc tcc tca    420
140    Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
141          130          135          140
143 <210> SEQ ID NO: 4
144 <211> LENGTH: 140
145 <212> TYPE: PRT

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146 <213> ORGANISM: Mus musculus
147 <220> FEATURE:
148 <221> NAME/KEY: SIGNAL
149 <222> LOCATION: (1)...(19)
150 <223> OTHER INFORMATION: signal peptide
151 <220> FEATURE:
152 <221> NAME/KEY: SITE
153 <222> LOCATION: (20)...(49)
154 <223> OTHER INFORMATION: framework 1
155 <220> FEATURE:
156 <221> NAME/KEY: SITE
157 <222> LOCATION: (50)...(54)
158 <223> OTHER INFORMATION: CDR1
159 <220> FEATURE:
160 <221> NAME/KEY: SITE
161 <222> LOCATION: (55)...(68)
162 <223> OTHER INFORMATION: framework 2
163 <220> FEATURE:
164 <221> NAME/KEY: SITE
165 <222> LOCATION: (69)...(85)
166 <223> OTHER INFORMATION: CDR2
167 <220> FEATURE:
168 <221> NAME/KEY: SITE
169 <222> LOCATION: (86)...(117)
170 <223> OTHER INFORMATION: framework 3
171 <220> FEATURE:
172 <221> NAME/KEY: SITE
173 <222> LOCATION: (118)...(129)
174 <223> OTHER INFORMATION: CDR3
175 <220> FEATURE:
176 <221> NAME/KEY: SITE
177 <222> LOCATION: (130)...(140)
178 <223> OTHER INFORMATION: framework 4
179 <400> SEQUENCE: 4
180 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
181 1 5 10 15
182 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
183 20 25 30
184 Pro Gly Thr Ser Val Lys Leu Ser Cys Lys Gly Tyr Gly Tyr Thr Phe
185 35 40 45
186 Thr Ser Tyr Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
187 50 55 60
188 Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
189 65 70 75 80
190 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Ile Ser Ser Ser
191 85 90 95
192 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
193 100 105 110
194 Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp

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195          115          120          125
196      Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
197          130          135          140
199 <210> SEQ ID NO: 5
200 <211> LENGTH: 540
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Portion of the heavy chain of LDP-02 with a heavy
205     chain signal peptide
206 <220> FEATURE:
207 <221> NAME/KEY: CDS
208 <222> LOCATION: (1)...(540)
209 <400> SEQUENCE: 5
210      atg aaa tgc acc tgg gtc att ctc ttc ttg gta tca aca gct aca agt   48
211      Met Lys Cys Thr Trp Val Ile Leu Phe Leu Val Ser Thr Ala Thr Ser
212          1          5          10          15
213      gtc cac tcc cag gtc caa cta gtg cag tct ggg gct gag gtt aag aag   96
214      Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
215          20          25          30
216      cct ggg gct tca gtg aag gtg tcc tgc aag ggt tct ggc tac acc ttc   144
217      Pro Gly Ala Ser Val Lys Val Ser Cys Lys Gly Ser Gly Tyr Thr Phe
218          35          40          45
219      acc agc tac tgg atg cat tgg gtg agg cag gcg cct ggc caa cgt cta   192
220      Thr Ser Tyr Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
221          50          55          60
222      gag tgg atc gga gag att gat cct tct gag agt aat act aac tac aat   240
223      Glu Trp Ile Gly Glu Ile Asp Pro Ser Glu Ser Asn Thr Asn Tyr Asn
224          65          70          75          80
225      caa aaa ttc aag gga cgc gtc aca ttg act gta gac att tcc gct agc   288
226      Gln Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Ile Ser Ala Ser
227          85          90          95
228      aca gcc tac atg gag ctc agc agc ctg aga tct gag gac act gcg gtc   336
229      Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
230          100          105          110
231      tac tat tgt gca aga ggg ggt tac gac gga tgg gac tat gct att gac   384
232      Tyr Tyr Cys Ala Arg Gly Gly Tyr Asp Gly Trp Asp Tyr Ala Ile Asp
233          115          120          125
234      tac tgg ggt caa ggc acc ctg gtc acc gtc tcc tca gcc tcc acc aag   432
235      Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
236          130          135          140
237      ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg   480
238      Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
239          145          150          155          160
240      ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg   528
241      Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
242          165          170          175
243      gtg acg gtg tcg                                     540
244      Val Thr Val Ser

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VERIFICATION SUMMARY

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